Serial Number: 09/889,314

ENTERED

CRF Processing Dat : 1/17/2002 #5
Edited by: _____
V rified by: _____ (STIC staff)

DC

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was wrapped down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: Corrected <1407, <1417, <1507, <1517 sections

_____

_____

*Examiner: The above corrections must b communicated to th applicant in the first Office
Action. DO NOT send a copy of this form.

3/1/95

```
                RAW SEQUENCE LISTING                DATE: 01/17/2002
                PATENT APPLICATION:  US/09/889,314  TIME: 08:04:08

                Input Set : A:\PTO.AMC.txt
                Output Set: N:\CRF3\01172002\I889314.raw
```

```
 3 <110> APPLICANT: BURNIE, JAMES PETER
 4        MATTHEWS, RUTH CHRISTINE
 6 <120> TITLE OF INVENTION: MEDICAMENT
 8 <130> FILE REFERENCE: 050885-0281578
10 <140> CURRENT APPLICATION NUMBER: 09/889,314
11 <141> CURRENT FILING DATE: 2001-07-16
13 <150> PRIOR APPLICATION NUMBER: GB 9902555.3
14 <151> PRIOR FILING DATE: 1999-02-05
16 <150> PRIOR APPLICATION NUMBER: PCT/GB00/00237
17 <151> PRIOR FILING DATE: 2000-01-28
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1491
26 <212> TYPE: DNA
27 <213> ORGANISM: Chlamydia pneumoniae
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1491)
33 <400> SEQUENCE: 1
34 gat aca aac atg tct att tca tct tct tca gga cct gac aat caa aaa    48
35 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
36   1               5                  10                  15
38 aat atc atg tct caa gtt ctg aca tcg aca ccc cag ggc gtg ccc caa    96
39 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
40               20                  25                  30
42 caa gat aag ctg tct ggc aac gaa acg aag caa ata cag caa aca cgt   144
43 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
44           35                  40                  45
46 cag ggt aaa aac act gag atg gaa agc gat gcc act att gct ggt gct   192
47 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
48           50                  55                  60
50 tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca   240
51 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
52   65                  70                  75                  80
54 caa cag gga gtt gct gct ggg aaa gaa tcc tca gaa agt caa aag gca   288
55 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
56               85                  90                  95
58 ggt gct gat act gga gta tca gga gcg gct gct act aca gca tca aat   336
59 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
60               100                 105                 110
62 act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa   384
63 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
64           115                 120                 125
66 agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa   432
67 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
68           130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 01/17/2002
PATENT APPLICATION: US/09/889,314   TIME: 08:04:08

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Output Set: N:\CRF3\01172002\I889314.raw

```
70  atg aaa gaa gtc gaa gcg gtt gtt gtt gct gcc ctc tca ggg aaa agt   480
71  Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
72  145             150             155             160
74  tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg   528
75  Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
76              165             170             175
78  aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca   576
79  Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
80              180             185             190
82  att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca   624
83  Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
84          195             200             205
86  agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag   672
87  Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
88      210             215             220
90  caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag   720
91  Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
92  225             230             235             240
94  gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc   768
95  Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
96              245             250             255
98  aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att   816
99  Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
100             260             265             270
102 gtt gct gct att ttt aca tgc gga gct gga ctc gct gga ctc gct gcg   864
103 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
104         275             280             285
106 gga gct gct gta ggt gca gcg gca gct gga ggt gca gca gga gct gct   912
107 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
108     290             295             300
110 gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa   960
111 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
112 305             310             315             320
114 gcg gtg aaa caa gct gtt atc aca gct gtc aga caa gcg atc acc gcg   1008
115 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
116             325             330             335
118 gct ata aaa gcg gct gtc aaa tct gga ata aaa gca ttt atc aaa act   1056
119 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
120         340             345             350
122 tta gtc aaa gcg att gcc aaa gcc att tct aaa gga atc tct aag gtt   1104
123 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
124         355             360             365
126 ttc gct aag gga act caa atg att gcg aag aac ttc ccc aag ctc tcg   1152
127 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
128     370             375             380
130 aaa gtc atc tcg tct ctt acc agt aaa tgg gtc acg gtt ggg gtt ggg   1200
131 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
132 385             390             395             400
134 gtt gta gtt gcg gcg cct gct ctc ggt aaa ggg att atg caa atg cag   1248
```

RAW SEQUENCE LISTING   DATE: 01/17/2002
PATENT APPLICATION: US/09/889,314   TIME: 08:04:08

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\01172002\I889314.raw

```
135 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
136             405             410             415
138 ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga    1296
139 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
140             420             425             430
142 aaa ctg cag gct gcg gct gat atg att tct atg ttc act caa ttt tgg    1344
143 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
144         435             440             445
146 caa cag gca agt aaa att gcc tca aaa caa aca ggc gag tct aat gaa    1392
147 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
148         450             455             460
150 atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gcg tat    1440
151 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
152 465             470             475             480
154 gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt    1488
155 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
156             485             490             495
158 taa                                                                1491
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 496
164 <212> TYPE: PRT
165 <213> ORGANISM: Chlamydia pneumoniae
167 <400> SEQUENCE: 2
168 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
169 1               5               10              15
171 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
172             20              25              30
174 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
175         35              40              45
177 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
178     50              55              60
180 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
181 65              70              75              80
183 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
184             85              90              95
186 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
187         100             105             110
189 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
190         115             120             125
192 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
193         130             135             140
195 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
196 145             150             155             160
198 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
199             165             170             175
201 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
202         180             185             190
204 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
205         195             200             205
```

RAW SEQUENCE LISTING   DATE: 01/17/2002
PATENT APPLICATION: US/09/889,314   TIME: 08:04:08

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\01172002\I889314.raw

```
207 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
208     210                 215                 220
210 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
211 225             230                 235                 240
213 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
214             245                 250                 255
216 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
217         260                 265                 270
219 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
220         275                 280                 285
222 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
223         290                 295                 300
225 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
226 305                 310                 315                 320
228 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
229             325                 330                 335
231 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
232             340                 345                 350
234 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
235             355                 360                 365
237 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
238         370                 375                 380
240 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
241 385                 390                 395                 400
243 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
244             405                 410                 415
246 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
247         420                 425                 430
249 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
250         435                 440                 445
252 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
253     450                 455                 460
255 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
256 465                 470                 475                 480
258 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
259             485                 490                 495
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 302
264 <212> TYPE: PRT
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Description of Artificial Sequence: Codon
269       optimised N-terminal section of Chlamydia
270       pneumoniae protein
272 <220> FEATURE:
273 <221> NAME/KEY: UNSURE
274 <222> LOCATION: (1)..(30)
275 <223> OTHER INFORMATION: S-tag and thrombin cleavage site
277 <220> FEATURE:
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278 <223> OTHER INFORMATION: Positions (297)..(302) comprise Histidine tag
280 <400> SEQUENCE: 3
281 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
282 1   5   10   15
284 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Ala Ile Ser Asp Pro
285   20   25   30
287 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
288   35   40   45
290 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
291   50   55   60
293 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
294 65   .   70   75   80
296 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
297   85   90   95
299 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
300   100   105   110
302 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
303   115   120   125
305 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
306   130   135   140
308 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
309 145   150   155   160
311 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
312   165   170   175
314 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
315   180   185   190
317 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
318   195   200   205
320 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
321   210   215   220
323 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
324 225   230   235   240
326 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
327   245   250   255
329 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
330   260   265   270
332 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
333   275   280   285
335 Asn Thr Val Ala Ala Ala Leu Glu His His His His His His
336   290   295   300
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 9
341 <212> TYPE: PRT
342 <213> ORGANISM: Chlamydia pneumoniae
344 <400> SEQUENCE: 4
345 Ser Ala Lys Leu Glu Thr Pro Glu Leu
346 1   5
349 <210> SEQ ID NO: 5
350 <211> LENGTH: 7

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/889,314

DATE: 01/17/2002
TIME: 08:04:09

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\01172002\I889314.raw**